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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/088,549A

DATE: 12/13/2002

TIME: 13:47:03

Input Set : A:\DEBE007US.txt

Output Set: N:\CRF4\12132002\J088549A.raw

P.6

3 <110> APPLICANT: Erik Nielsen
 4 Savvas Chritophoridis
 5 Carol Murphy
 6 Marino Zerial
 7 Stefano De Renzis
 9 <120> TITLE OF INVENTION: ASSAY TO DETECT SUBSTANCES USEFUL FOR THERAPY
 11 <130> FILE REFERENCE: DEBE:007US
 13 <140> CURRENT APPLICATION NUMBER: 10/088,549A
 C--> 14 <141> CURRENT FILING DATE: 2002-08-02
 16 <150> PRIOR APPLICATION NUMBER: PCT/EP 00/09130
 17 <151> PRIOR FILING DATE: 2000-09-18
 19 <150> PRIOR APPLICATION NUMBER: EP 99 118 385.6
 20 <151> PRIOR FILING DATE: 1999-09-16
 22 <160> NUMBER OF SEQ ID NOS: 16
 24 <170> SOFTWARE: PatentIn Ver. 2.1
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 3510
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Homo sapiens
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 34 gcaaacaagg agagcagcag cgagtccttc atcagccgtc tgctggccat cgtggcagac 180
 35 ctctacgagc aggagcagta cagcgatctg aagataaaagg ttggggacag gcacatcagt 240
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 37 actaaagagt tggacctgtc cgatgctaat cctgaggtga cgatgacaat gcttcgctgg 360
 38 atctatacag atgagcttgg a g t c a g a g a g a g a t g a t g t g t c t c t g a c t g a a a a 420
 39 ctagcaaatac gtttcagct acagctcctc agggagagat gtgagaaggg t g t t a t g t c t 480
 40 ctagtgaatg tcaggaactg tatttcgttcc taccagacgg cagaggagct gaatgccagc 540
 41 acattgtatgactactgtgc agaaattattt gcaagtcatt gggacgacct gaggaaggag 600
 42 gatttcagca gcatgagcgc tcagttgtta tacaaaatga tcaaattccaa gacagagttac 660
 43 ccgttacata aagccatcaa a g t g g a g a g a g a a g a c g t g g t c t c t g t a t c t g a t t g a a 720
 44 atggattccc agtccctgg gaagctgaat g a a g c g g a t c a t a a c g g a g a g a t c t g g c a t t a 780
 45 gatctagccc tttcacgacg actggagagt attgcccacca cgctggtag tcacaaagct 840
 46 gatgtggaca tggggacaa g a g t g g c t g g a g c t t g t a c a c a a g g a a t c c a a a g g a g g a 900
 47 gatctctttc ctgccactt c c t c t t a a g a a t g g g g c t t g t c a a c g c t g a c t g 960
 48 ggtgcccagg agacaccact g c a c c t t g t g c t t g t a c a g t c a a a g g a a a c a c t c a g g a 1020
 49 gatgtatgtt c t g a g a t g g c g c a g a t t g c a g a g c c t t c t g c a g g c t g g t g c c a a c c c 1080
 50 aacatgcagg acagcaaggg g a g g a c t c c t t a c a t g t g t c c a t c a t g g c c g g a a t g a a 1140
 51 tatgtgttca g t c a g c t g c t g c a g t g c a a a a c a a t g a a t t g a a c t c a a a g a c c a c g a g 1200
 52 ggcagcacgg ctctgtggct g g c a g t g c a g c a t a t c a c a g t g t c t g a c c a g t c t g t g 1260
 53 aacccttcg a a g a t g t c c c c t g g t a a a t g g a c t t c a t t g a t g a g a a a c a g c t t g c a 1320
 54 gccagactca t c c a g c g c g g c a g c a c a c a g a c a c t g a c a c g g c g a c a g g a a c t g t 1380

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55 ttactacagc gggcagctgg agcaggaaac gaggcagcag ctctttcct ggcaaccaac 1440
 56 ggtgcccattt tcaaccacag aaacaagtgg ggagaaaccc cggtgcacac agcgtgtcgg 1500
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 60 gtcatcctgg agcagaaagc caatgtctt catgcacca acaacttgc a gatcattccg 1740
 61 gacttcagcc tcaaagattt ccgagaccag actgtgtcgg gcctggcattt atggactggc 1800
 62 atgcacacga tcgcagccca gctgctggc tctggagctg ccatcaatga caccatgtcg 1860
 63 gatggcaga cgctactgca catggccata cagcggcagg acagcaagag cgcaacttcc 1920
 64 ctgctggagc accaggcaga tataaatgtc aggactcagg acggggagac agccctccag 1980
 65 ctggccatca gaaaccagct tccactcgta gttgtatgcca tatgcacccg aggagctgac 2040
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 68 cctgggtgggt gccttcagac gctcctgcac agagccattt atgaaaacaa cgagccacc 2220
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 70 ggagaaggag aggaaggagc tagagatggg cagaccctt tgcatttggc agccttgg 2340
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 72 gcaagaaggaa gaaccccat ccacgtggcc atcagcagcc aacacgggtt catcattcag 2460
 73 ctgttgggtt ctcaccccgaa tatccattt aatgtacgag acagacaagg gctgaccccg 2520
 74 tttgcctgtg ccatgacttt caagaacaaac aagtcaagccg aggccattt caaacgagag 2580
 75 tccggggctg ctgagcagggt ggataacaag ggccgaatt tccttcatgt ggcagttcag 2640
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 77 gtccaggatg cctccaagtt gaccccccctg caccctcgctg tccaaaggcagg ctcagaaatt 2760
 78 attgtccgca atttgcttctg tgcgggagcc aaagtgaacg aattaaccaa gcatcgccag 2820
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 81 atgcacggcc ggctcaacaa catccgggtt ctcctgacag a g t g c a c a g t ggacgcccga 3000
 82 gcctttaatc tcagaggcca gtcaccactg cacatttgg gacaatatgg caaggagaat 3060
 83 gcagcggcca tctttgatct cttcttagaa tgcatggccg ggtatcctt ggacaagccg 3120
 84 gatgcagacg gcagcacggt gctgttcttgc gcatacatga aagggAACgc caacattgtgc 3180
 85 cgcgcctatcg tccggcggg ggctcgctc ggggtgaata acaaccagg agtcaacatc 3240
 86 ttcaactacc aggtcgccac caagcagctc ctgttccgac tgctggatat gctgtccaag 3300
 87 gagctccgtt ggtgtgacgg ctctctactgc tatgagtgc ctgcccagggtt cggagtcacc 3360
 88 actcgcaaac accactgtcg tcaactgcggg cgtctttt gccataaaatg ctcgaccaag 3420
 89 gagattccta ttataaaagtgtt tgatctgaac aagcctgtgc gggtttgc aa catttgc 3480
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93 <210> SEQ ID NO: 2

94 <211> LENGTH: 1169

95 <212> TYPE: PRT

96 <213> ORGANISM: Homo sapiens

98 <400> SEQUENCE: 2

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 100 1 5 10 15
 102 Arg Gln Glu Tyr Val Lys Leu Gln Lys Lys Leu Ala Glu Thr Glu Lys
 103 20 25 30
 105 Arg Cys Ala Leu Leu Ala Ala Gln Ala Asn Lys Glu Ser Ser Ser Glu
 106 35 40 45
 108 Ser Phe Ile Ser Arg Leu Leu Ala Ile Val Ala Asp Leu Tyr Glu Gln
 109 50 55 60

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111 Glu Gln Tyr Ser Asp Leu Lys Ile Lys Val Gly Asp Arg His Ile Ser
112 65 70 75 80
114 Ala His Lys Phe Val Leu Ala Ala Arg Ser Asp Ser Trp Ser Leu Ala
115 85 90 95
117 Asn Leu Ser Ser Thr Lys Glu Leu Asp Leu Ser Asp Ala Asn Pro Glu
118 100 105 110
120 Val Thr Met Thr Met Leu Arg Trp Ile Tyr Thr Asp Glu Leu Glu Phe
121 115 120 125
123 Arg Glu Asp Asp Val Phe Leu Thr Glu Leu Met Lys Leu Ala Asn Arg
124 130 135 140
126 Phe Gln Leu Gln Leu Leu Arg Glu Arg Cys Glu Lys Gly Val Met Ser
127 145 150 155 160
129 Leu Val Asn Val Arg Asn Cys Ile Arg Phe Tyr Gln Thr Ala Glu Glu
130 165 170 175
132 Leu Asn Ala Ser Thr Leu Met Asn Tyr Cys Ala Glu Ile Ile Ala Ser
133 180 185 190
135 His Trp Asp Asp Leu Arg Lys Glu Asp Phe Ser Ser Met Ser Ala Gln
136 195 200 205
139 Leu Leu Tyr Lys Met Ile Lys Ser Lys Thr Glu Tyr Pro Leu His Lys
140 210 215 220
142 Ala Ile Lys Val Glu Arg Glu Asp Val Val Phe Leu Tyr Leu Ile Glu
143 225 230 235 240
145 Met Asp Ser Gln Leu Pro Gly Lys Leu Asn Glu Ala Asp His Asn Gly
146 245 250 255
148 Asp Leu Ala Leu Asp Leu Ala Leu Ser Arg Arg Leu Glu Ser Ile Ala
149 260 265 270
151 Thr Thr Leu Val Ser His Lys Ala Asp Val Asp Met Val Asp Lys Ser
152 275 280 285
154 Gly Trp Ser Leu Leu His Lys Gly Ile Gln Arg Gly Asp Leu Phe Ala
155 290 295 300
157 Ala Thr Phe Leu Ile Lys Asn Gly Ala Phe Val Asn Ala Ala Thr Leu
158 305 310 315 320
160 Gly Ala Gln Glu Thr Pro Leu His Leu Val Ala Leu Tyr Ser Ser Lys
161 325 330 335
163 Lys His Ser Ala Asp Val Met Ser Glu Met Ala Gln Ile Ala Glu Ala
164 340 345 350
166 Leu Leu Gln Ala Gly Ala Asn Pro Asn Met Gln Asp Ser Lys Gly Arg
167 355 360 365
169 Thr Pro Leu His Val Ser Ile Met Ala Gly Asn Glu Tyr Val Phe Ser
170 370 375 380
172 Gln Leu Leu Gln Cys Lys Gln Leu Asp Leu Glu Leu Lys Asp His Glu
173 385 390 395 400
175 Gly Ser Thr Ala Leu Trp Leu Ala Val Gln His Ile Thr Val Ser Ser
176 405 410 415
178 Asp Gln Ser Val Asn Pro Phe Glu Asp Val Pro Val Val Asn Gly Thr
179 420 425 430
181 Ser Phe Asp Glu Asn Ser Phe Ala Ala Arg Leu Ile Gln Arg Gly Ser
182 435 440 445
183 His Thr Asp Ala Pro Asp Thr Ala Thr Gly Asn Cys Leu Leu Gln Arg

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184	450	455	460													
186	Ala	Ala	Gly	Ala	Gly	Asn	Glu	Ala	Ala	Ala	Leu	Phe	Leu	Ala	Thr	Asn
187	465	470	475	480												
189	Gly	Ala	His	Val	Asn	His	Arg	Asn	Lys	Trp	Gly	Glu	Thr	Pro	Leu	His
190	485	490	495													
192	Thr	Ala	Cys	Arg	His	Gly	Leu	Ala	Asn	Leu	Thr	Ala	Glu	Leu	Leu	Gln
193	500	505	510													
195	Gln	Gly	Ala	Asn	Pro	Asn	Leu	Gln	Thr	Glu	Glu	Ala	Leu	Pro	Leu	Pro
196	515	520	525													
198	Lys	Glu	Ala	Ala	Ser	Leu	Thr	Ser	Leu	Ala	Asp	Ser	Val	His	Leu	Gln
199	530	535	540													
201	Thr	Pro	Leu	His	Met	Ala	Ile	Ala	Tyr	Asn	His	Pro	Asp	Val	Val	Ser
202	545	550	555	560												
204	Val	Ile	Leu	Glu	Gln	Lys	Ala	Asn	Ala	Leu	His	Ala	Thr	Asn	Asn	Leu
205	565	570	575													
207	Gln	Ile	Ile	Pro	Asp	Phe	Ser	Leu	Lys	Asp	Ser	Arg	Asp	Gln	Thr	Val
208	580	585	590													
210	Leu	Gly	Leu	Ala	Leu	Trp	Thr	Gly	Met	His	Thr	Ile	Ala	Gln	Leu	
211	595	600	605													
213	Leu	Gly	Ser	Gly	Ala	Ala	Ile	Asn	Asp	Thr	Met	Ser	Asp	Gly	Gln	Thr
214	610	615	620													
216	Leu	Leu	His	Met	Ala	Ile	Gln	Arg	Gln	Asp	Ser	Lys	Ser	Ala	Leu	Phe
217	625	630	635	640												
219	Leu	Leu	Glu	His	Gln	Ala	Asp	Ile	Asn	Val	Arg	Thr	Gln	Asp	Gly	Glu
220	645	650	655													
222	Thr	Ala	Leu	Gln	Leu	Ala	Ile	Arg	Asn	Gln	Leu	Pro	Leu	Val	Val	Asp
223	660	665	670													
225	Ala	Ile	Cys	Thr	Arg	Gly	Ala	Asp	Met	Ser	Val	Pro	Asp	Glu	Lys	Gly
226	675	680	685													
227	Asn	Pro	Pro	Leu	Trp	Leu	Ala	Leu	Ala	Asn	Asn	Leu	Glu	Asp	Ile	Ala
228	690	695	700													
230	Ser	Thr	Leu	Val	Arg	His	Gly	Cys	Asp	Ala	Thr	Cys	Trp	Gly	Pro	Gly
231	705	710	715	720												
233	Pro	Gly	Gly	Cys	Leu	Gln	Thr	Leu	Leu	His	Arg	Ala	Ile	Asp	Glu	Asn
234	725	730	735													
236	Asn	Glu	Pro	Thr	Ala	Cys	Phe	Leu	Ile	Arg	Ser	Gly	Cys	Asp	Val	Asn
237	740	745	750													
239	Ser	Pro	Arg	Gln	Pro	Gly	Ala	Asn	Gly	Glu	Gly	Glu	Glu	Ala	Arg	
240	755	760	765													
242	Asp	Gly	Gln	Thr	Pro	Leu	His	Leu	Ala	Ala	Ser	Trp	Gly	Leu	Glu	
243	770	775	780													
245	Thr	Val	Gln	Cys	Leu	Leu	Glu	Phe	Gly	Ala	Asn	Val	Asn	Ala	Gln	Asp
246	785	790	795	800												
248	Ala	Glu	Gly	Arg	Thr	Pro	Ile	His	Val	Ala	Ile	Ser	Ser	Gln	His	Gly
249	805	810	815													
251	Val	Ile	Ile	Gln	Leu	Leu	Val	Ser	His	Pro	Asp	Ile	His	Leu	Asn	Val
252	820	825	830													
254	Arg	Asp	Arg	Gln	Gly	Leu	Thr	Pro	Phe	Ala	Cys	Ala	Met	Thr	Phe	Lys
255	835	840	845													

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257 Asn Asn Lys Ser Ala Glu Ala Ile Leu Lys Arg Glu Ser Gly Ala Ala
 258 850 855 860
 260 Glu Gln Val Asp Asn Lys Gly Arg Asn Phe Leu His Val Ala Val Gln
 261 865 870 875 880
 263 Asn Ser Asp Ile Glu Ser Val Leu Phe Leu Ile Ser Val His Ala Asn
 264 885 890 895
 266 Val Asn Ser Arg Val Gln Asp Ala Ser Lys Leu Thr Pro Leu His Leu
 267 900 905 910
 269 Ala Val Gln Ala Gly Ser Glu Ile Ile Val Arg Asn Leu Leu Ala
 270 915 920 925
 271 Gly Ala Lys Val Asn Glu Leu Thr Lys His Arg Gln Thr Ala Leu His
 272 930 935 940
 274 Leu Ala Ala Gln Gln Asp Leu Pro Thr Ile Cys Ser Val Leu Leu Glu
 275 945 950 955 960
 277 Asn Gly Val Asp Phe Ala Ala Val Asp Glu Asn Gly Asn Asn Ala Leu
 278 965 970 975
 280 His Leu Ala Val Met His Gly Arg Leu Asn Asn Ile Arg Val Leu Leu
 281 980 985 990
 283 Thr Glu Cys Thr Val Asp Ala Glu Ala Phe Asn Leu Arg Gly Gln Ser
 284 995 1000 1005
 286 Pro Leu His Ile Leu Gly Gln Tyr Gly Lys Glu Asn Ala Ala Ala Ile
 287 1010 1015 1020
 289 Phe Asp Leu Phe Leu Glu Cys Met Pro Gly Tyr Pro Leu Asp Lys Pro
 290 1025 1030 1035 1040
 292 Asp Ala Asp Gly Ser Thr Val Leu Leu Ala Tyr Met Lys Gly Asn
 293 1045 1050 1055
 295 Ala Asn Leu Cys Arg Ala Ile Val Arg Ser Gly Ala Arg Leu Gly Val
 296 1060 1065 1070
 298 Asn Asn Asn Gln Gly Val Asn Ile Phe Asn Tyr Gln Val Ala Thr Lys
 299 1075 1080 1085
 301 Gln Leu Leu Phe Arg Leu Leu Asp Met Leu Ser Lys Glu Pro Pro Trp
 302 1090 1095 1100
 304 Cys Asp Gly Ser Tyr Cys Tyr Glu Cys Thr Ala Arg Phe Gly Val Thr
 305 1105 1110 1115 1120
 307 Thr Arg Lys His His Cys Arg His Cys Gly Arg Leu Leu Cys His Lys
 308 1125 1130 1135
 310 Cys Ser Thr Lys Glu Ile Pro Ile Ile Lys Phe Asp Leu Asn Lys Pro
 311 1140 1145 1150
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 314 1155 1160 1165
 315 Ser
 318 <210> SEQ ID NO: 3
 319 <211> LENGTH: 3390
 320 <212> TYPE: DNA
 321 <213> ORGANISM: Homo sapiens
 323 <400> SEQUENCE: 3
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 325 gtcagctgc agaagaagct ggcggagaca gagaagcgct gcgctcttt ggctgcgcag 120
 326 gcaaacaagg agagcagcag cgagtccttc atcagccgtc tgctggccat cgtggcagac 180

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/088,549A

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Input Set : A:\DEBE007US.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; Xaa Pos. 398,488

VERIFICATION SUMMARY

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:729 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:384

L:747 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:480